

TTCTATCGAT	TGAATTC	CCCC	GGGGATC	CCTC	TAGAGAT	CCCC	TCGAC	CTCGA					50
CCCACGCGTC	CGCCGGG	CGG	CGGCTTT	TGGA	TTTTG	GGGGG	GCGGGG	ACCA					100
GCTGCGCGGC	GGCACC		ATG	TTC	CTA	GCC	ACT	CTG	TAC	TTC			140
			Met	Phe	Leu	Ala	Thr	Leu	Tyr	Phe			
			1				5						
GCG	CTG	CCA	CTC	CTG	GAT	TTG	CTG	ATG	TCC	GCC	GAG	GTG	179
Ala	Leu	Pro	Leu	Leu	Asp	Leu	Leu	Met	Ser	Ala	Glu	Val	
	10					15					20		
AGT	GGT	GGA	GAC	CGT	CTG	GAC	TGT	GTG	AAA	GCC	AGC	GAT	218
Ser	Gly	Gly	Asp	Arg	Leu	Asp	Cys	Val	Lys	Ala	Ser	Asp	
			25				30						
CAG	TGC	CTG	AAG	GAA	CAG	AGC	TGC	AGC	ACC	AAG	TAC	CGC	257
Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	
	35				40					45			
ACA	CTA	AGG	CAG	TGC	GTG	GCG	GGC	AAG	GAA	ACC	AAC	TTC	296
Thr	Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	
		50					55					60	
AGC	CTG	ACA	TCC	GGC	CTT	GAG	GCC	AAG	GAT	GAG	TGC	CGT	335
Ser	Leu	Thr	Ser	Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	
				65					70				
AGC	GCC	ATG	GAG	GCC	TTG	AAG	CAG	AAG	TCT	CTG	TAC	AAC	374
Ser	Ala	Met	Glu	Ala	Leu	Lys	Gln	Lys	Ser	Leu	Tyr	Asn	
	75					80					85		
TGC	CGC	TGC	AAG	CGG	GGC	ATG	AAG	AAA	GAG	AAG	AAT	TGT	413
Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	Lys	Asn	Cys	
			90					95					
CTG	CGT	ATC	TAC	TGG	AGC	ATG	TAC	CAG	AGC	CTG	CAG	GGA	452
Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly	
100					105					110			
AAT	GAC	CTC	CTG	GAA	GAT	TCC	CCG	TAT	GAG	CCG	GTT	AAC	491
Asn	Asp	Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val	Asn	
		115					120					125	

FIG. 1A



Footnote 105000

CCA	GAG	TCA	AGG	TCT	GTC	AGC	AAC	TGT	CTT	AAG	GAG	AAC	959
Pro	Glu	Ser	Arg	Ser	Val	Ser	Asn	Cys	Leu	Lys	Glu	Asn	
270						275					280		
TAC	GCA	GAC	TGC	CTC	CTG	GCC	TAC	TCG	GGA	CTG	ATT	GGC	998
Tyr	Ala	Asp	Cys	Leu	Leu	Ala	Tyr	Ser	Gly	Leu	Ile	Gly	
			285					290					
ACA	GTC	ATG	ACT	CCC	AAC	TAC	GTA	GAC	TCC	AGC	AGC	CTC	1037
Thr	Val	Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Ser	Ser	Leu	
295					300					305			
AGC	GTG	GCA	CCA	TGG	TGT	GAC	TGC	AGC	AAC	AGC	GGC	AAT	1076
Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn	
		310					315					320	
GAC	CTG	GAA	GAC	TGC	TTG	AAA	TTT	CTG	AAT	TTT	TTT	AAG	1115
Asp	Leu	Glu	Asp	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	
				325					330				
GAC	AAT	ACT	TGT	CTC	AAA	AAT	GCA	ATT	CAA	GCC	TTT	GGC	1154
Asp	Asn	Thr	Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	
	335					340					345		
AAT	GGC	TCA	GAT	GTG	ACC	ATG	TGG	CAG	CCA	GCC	CCT	CCA	1193
Asn	Gly	Ser	Asp	Val	Thr	Met	Trp	Gln	Pro	Ala	Pro	Pro	
			350					355					
GTC	CAG	ACC	ACC	ACT	GCC	ACC	ACT	ACC	ACT	GCC	TTC	CGG	1232
Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr	Thr	Ala	Phe	Arg	
360					365					370			
GTC	AAG	AAC	AAG	CCT	CTG	GGG	CCA	GCA	GGG	TCT	GAG	AAT	1271
Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu	Asn	
		375					380					385	
GAG	ATC	CCC	ACA	CAC	GTT	TTA	CCA	CCC	TGT	GCG	AAT	TTG	1310
Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	
				390					395				
CAG	GCT	CAG	AAG	CTG	AAA	TCC	AAT	GTG	TCG	GGT	AGC	ACA	1349
Gln	Ala	Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Ser	Thr	
	400					405					410		

FIG. 1C

CAC CTC TGT CTT TCT GAT AGT GAT TTC GGA AAG GAT GGT	1388
His Leu Cys Leu Ser Asp Ser Asp Phe Gly Lys Asp Gly	
415 420	
CTC GCT GGT GCC TCC AGC CAC ATA ACC ACA AAA TCA ATG	1427
Leu Ala Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met	
425 430 435	
GCT GCT CCT CCC AGC TGC AGT CTG AGC TCA CTG CCG GTG	1466
Ala Ala Pro Pro Ser Cys Ser Leu Ser Ser Leu Pro Val	
440 445 450	
CTG ATG CTC ACC GCC CTT GCT GCC CTG TTA TCT GTA TCG	1505
Leu Met Leu Thr Ala Leu Ala Ala Leu Leu Ser Val Ser	
455 460	
TTG GCA GAA ACG TCG TAGCTGCATC CGGGAAAACA GTATGAAAAG	1550
Leu Ala Glu Thr Ser	
465 468	
ACAAAAGAGA ACCAAGTATT CTGTCCCTGT CCTCTTGTAT ATCTGAAAAT	1600
CCAGTTTAA AAGCTCCGTT GAGAAGCAGT TTCACCCAAC TGGAACCTTT	1650
TCCTTGTTTT TAAGAAAGCT TGTGGCCCTC AGGGGCTTCT GTTGAAGAAC	1700
TGCTACAGGG CTAATTCCAA ACCCATAAGG CTCTGGGGCG TGGTGCGGCT	1750
TAAGGGGACC ATTTGCACCA TGTAAGCAA GCTGGGCTTA TCATGTGTTT	1800
GATGGTGAGG ATGGTAGTGG TGATGATGAT GGTAATTTTA ACAGCTTGAA	1850
CCCTGTTCTC TCTACTGGTT AGGAACAGGA GATACTATTG ATAAAGATTC	1900
TTCCATGTCT TACTCAGCAG CATTGCCTTC TGAAGACAGG CCCGCAGCCT	1950
AGTGTGAATG ACAAGTGGAG GTTGGCCTCA AGAGTGGACT TGGCAGACTC	2000
TACCTTGTAG TAATGTTTAC CTTTCCGTGT ATGGTCTCCA CAGAGTGTTT	2050
ATGTATTTAC AGACTGTTCT GTGATCCCCC AACAACAACA ACCACAAATT	2100
CCTTGGTCAC CTCCAAATGT AACCGGTCCT TTAGCCCAGT AGAGGAGGGT	2150
GGGTGTGGCC CTGGCACAGC TCCCGGATTG TTGATGGGCA CTCTCCTGAG	2200

FIG. 1D

CTTTGCTTGA GTGAGAAGCT GAATGTAGCT GAAAATCAAC TCTTCTTACA	2250
CTTAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2300
AAAAAAAAAA AAAAGGTTTA GGGATAACAG GGTAATGCGG CCGCGTCGAC	2350
CTGCAGAAGC TTGGCCGCCA TGGCCCAA	2378

**FIG. 1E**

↓  
MELATLYFALPLLDLLMSAEVSGDRLD CVKASDQCLKEQSCSTKYRTLRCVAGKETNE  
SLTSGLEAKDECRSAMEALKQKSLYNCRCKRGMKKEKNCLRIYWSMYQSLQGNDLLEDSP  
 YEPVNSRLSDIFRAVPFISDVFQQVEHISKGNCLDAAKACNLDDTCKKYRSAYITPCTT  
 SMSNEVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCRDIACTERRRQTIVPVCSYEERER  
 PNCLSLQDSCKTNYICRSRLADFFTNCPESRSVSNCLKENYADCLLAYSGLIGTVMTPN  
 YVDSSSLSVAPWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQAFGNGSDVTMWQPAPPV  
 QTTTATTTAFRVKNKPLGPAGSENEIPTHVLPPCANLQAQKLKSNVSGSTHLC LSDSDF  
 GKDGLAGASSHITTKSMAAPPSCSLSSLPLMLTALAALLSVSLAETS

FIG. 2

SDS-PAGE gel showing GDNF + GDNFR $\alpha$  and GDNF lanes across four lanes (1-4). Molecular weight markers are indicated on the right: 200, 144, 87, 44.1, 33.7, 17, and 7.1 kDa. Arrows point to bands in lane 1.

FIG. 3

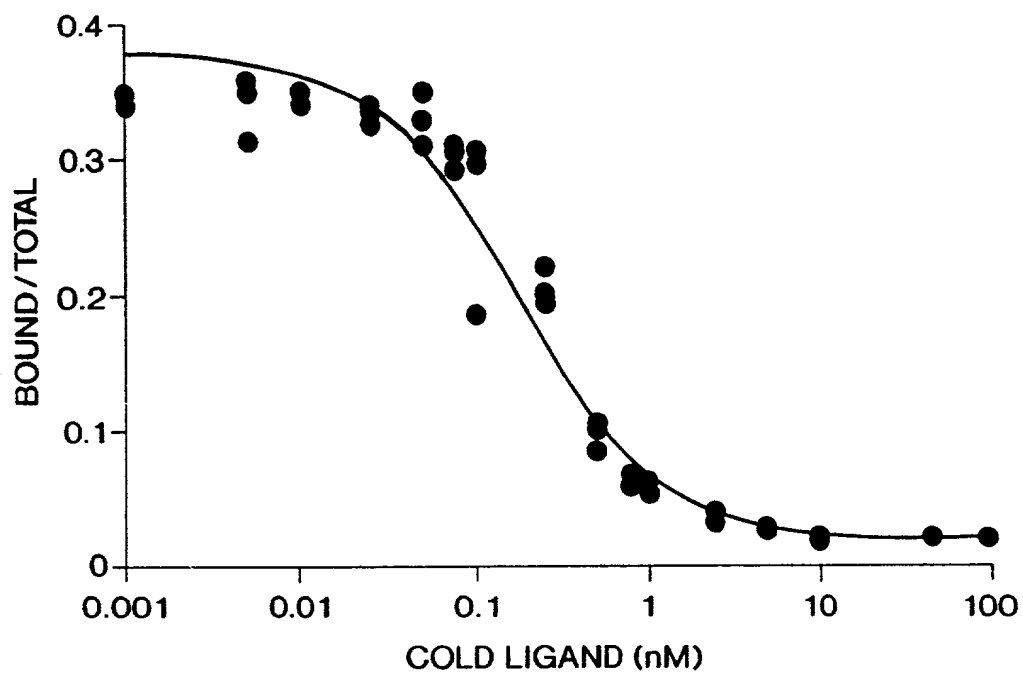


FIG. 4A

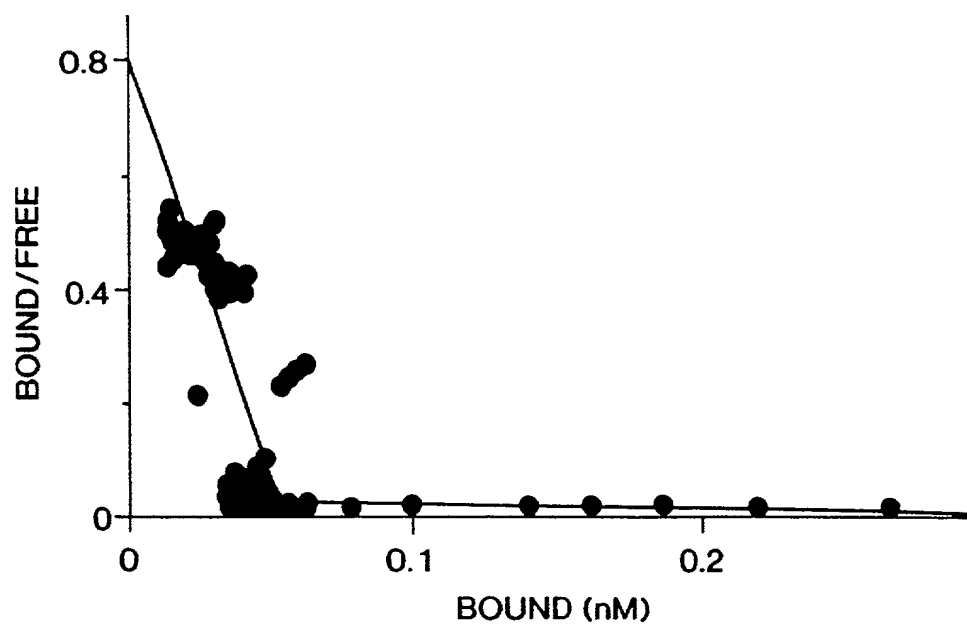


FIG. 4B



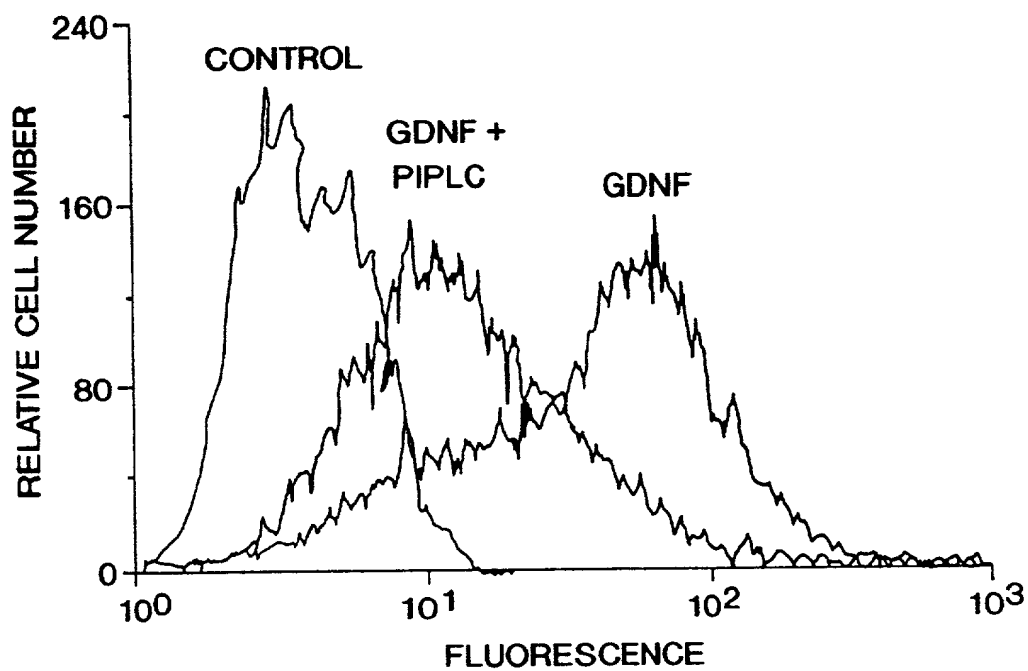


FIG. 5

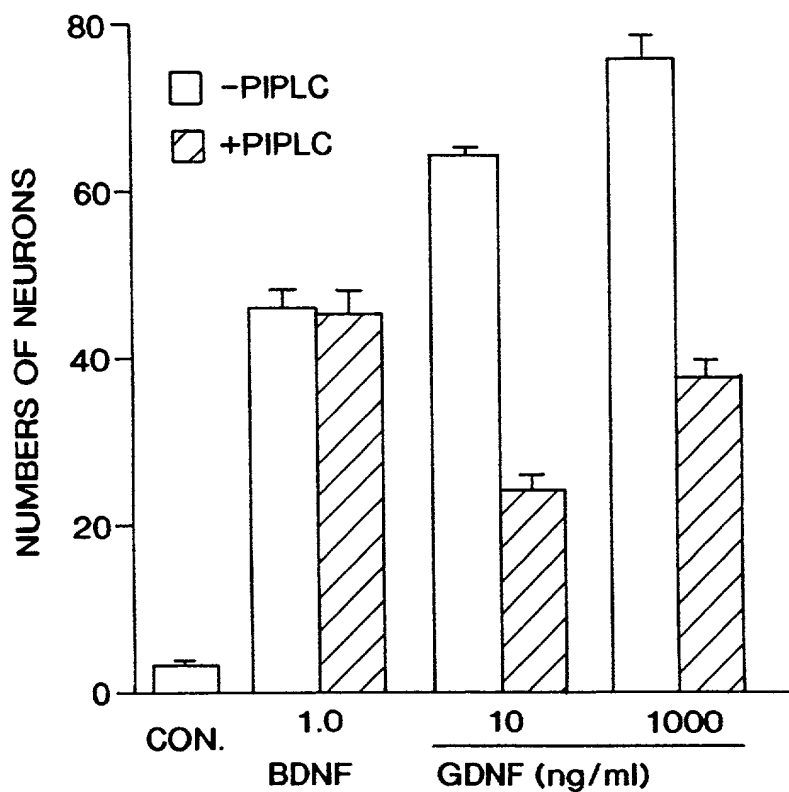


FIG. 6

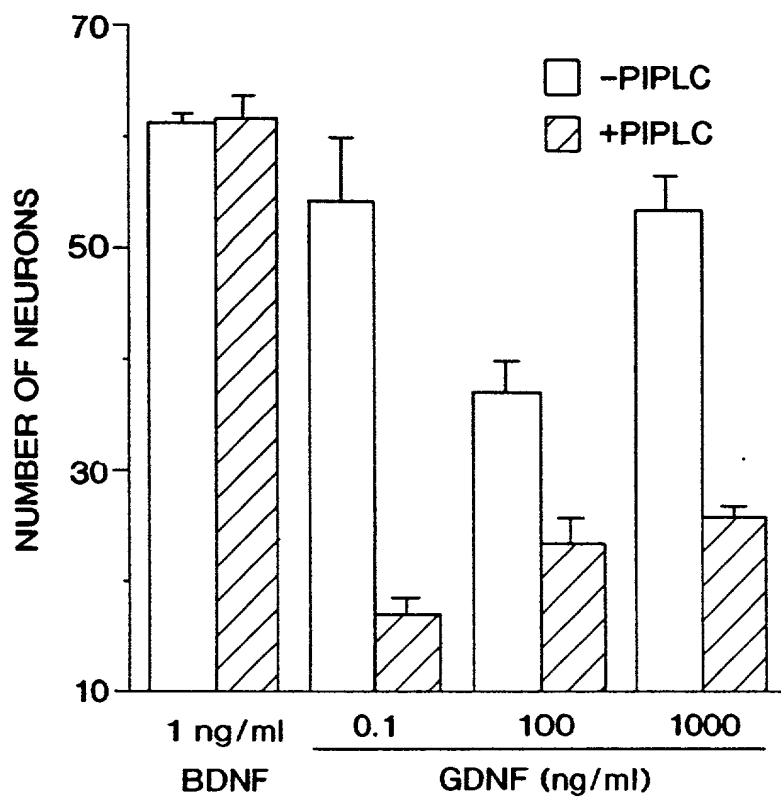


FIG. 7

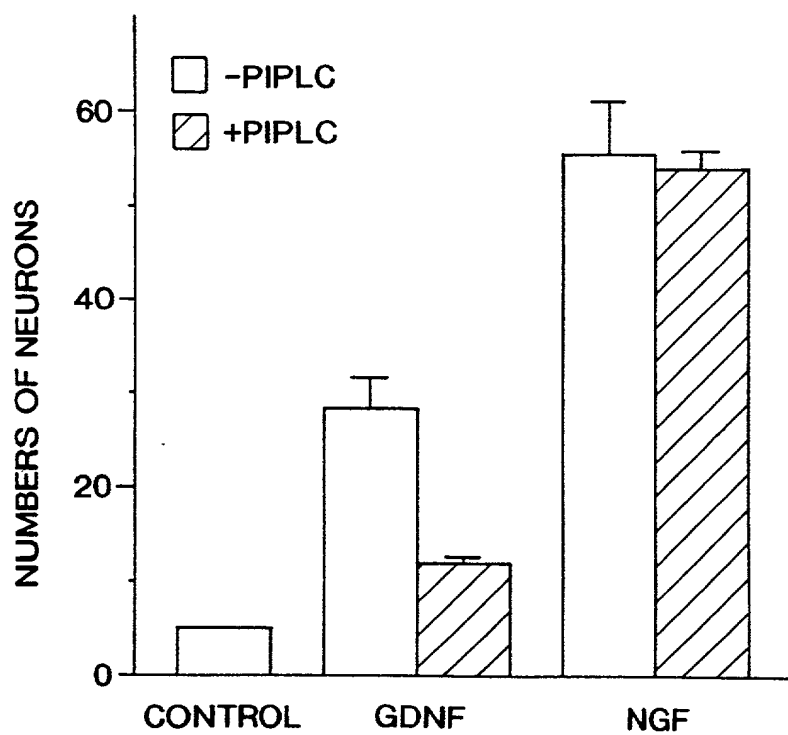
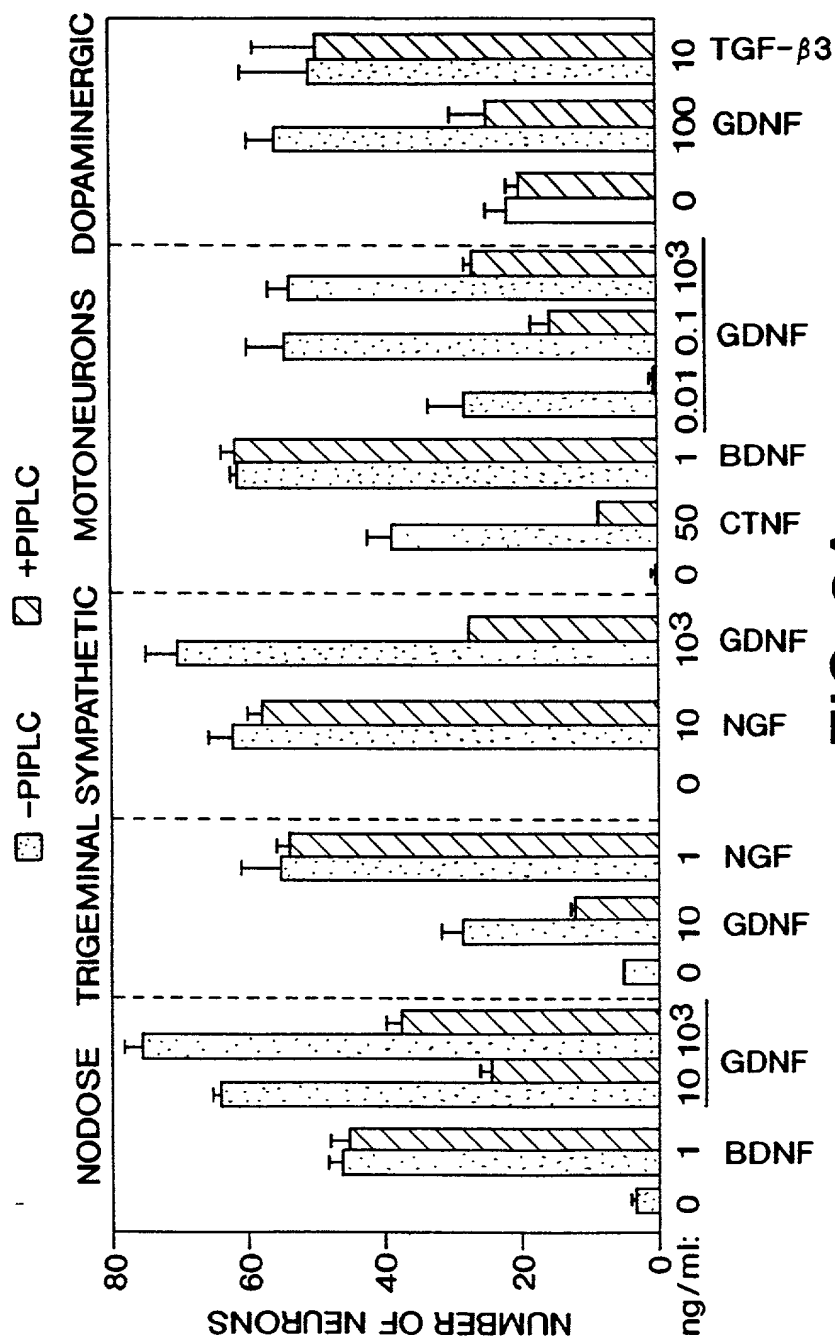


FIG. 8



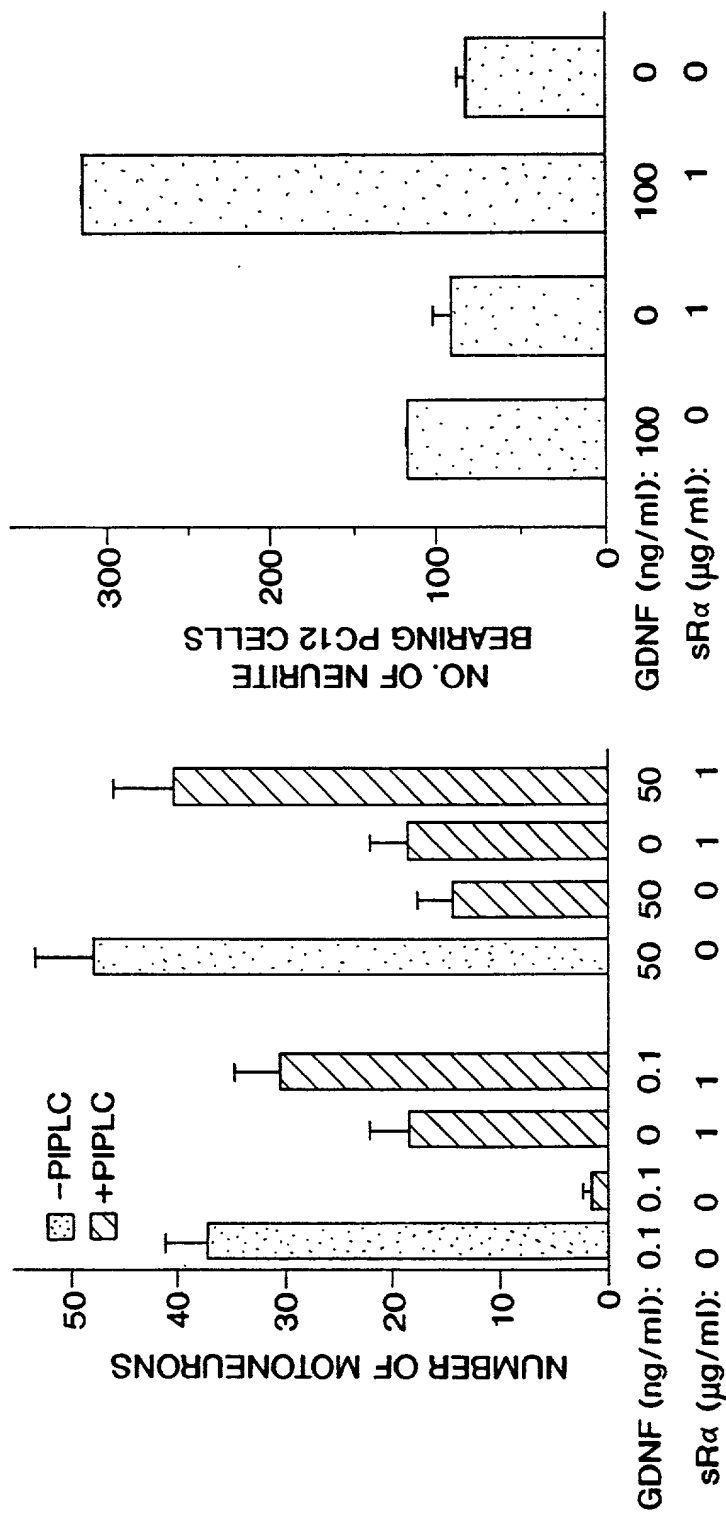


FIG. 9C

FIG. 9B

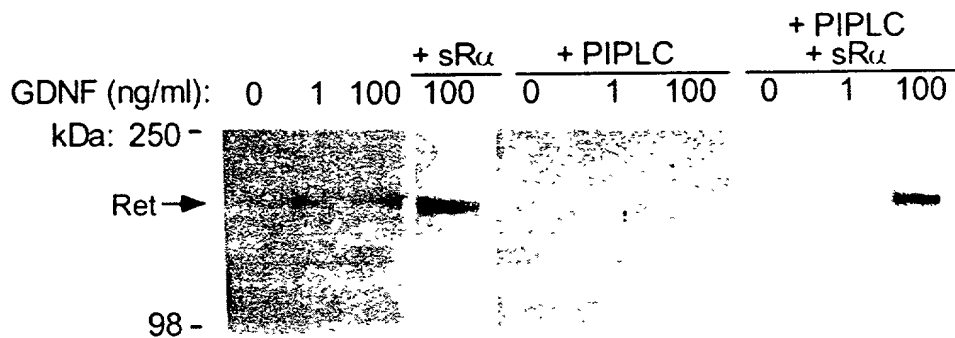


FIG. 10A

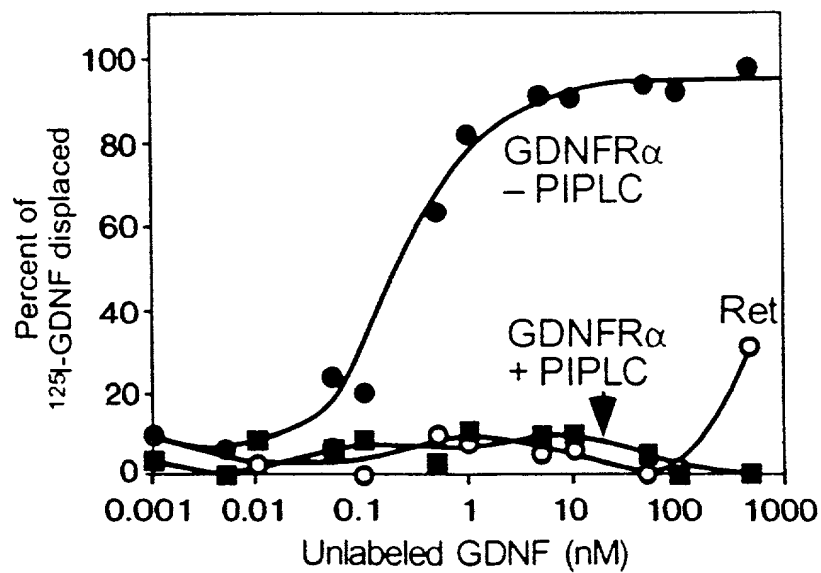


FIG. 10B

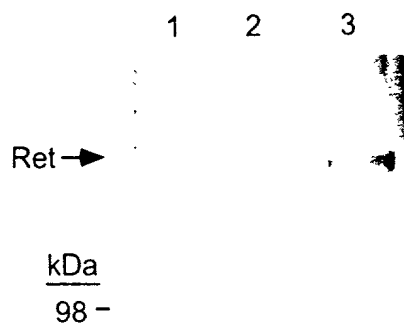


FIG. 10C

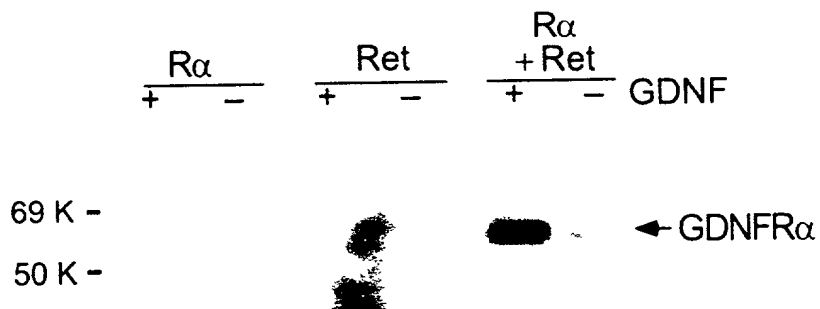


FIG. 10D